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CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT 903  
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr  
220 225 230

FIG. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

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TAGATGAGTC	TTGCTCTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAAACCATTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCCTTTGGGA	1749
TTCTTTGTAT	AGAGTCTCTG	AAAGAGAAAA	AGAGAAAAAG	TTTGGAACTC	CATCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAA	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTCG	TTATAAGCTG	ATTTACTGAA	ATCCCAATAAC	1929
CCATCAATGC	TGTTAATTTT	TTTCTTCTTA	CCCTTATTAC	ATTCCCTACC	TCAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTTATTGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

FIG. 1 (cont'd.)

[illegible]

deaNTase 1 ----MELLKNTFFLPCPAISSSOYONHULTSRPFKCEISASVAVFDAGSTGSR  
 potapyrase 1 RLNQNSHRPFIHLAMFLVGLSLSKMNAQFDRRHLSHSE..EYAVEFDAGSTGSR  
 mNTase 1 KATSWGKTFMHLACVGTTFYRFOOTFEGOTSSMCPNVSAGTFYQINFDAGSTGSR  
 yGDPase 1 KTFKHLTFPNDPFGLODAKTEORNFELADAKSQTSQTCSEKRYVIFIDAGSTGSR

deaNTase 57 LHVYRPNOMLDLHIGKOVETKXIFGLSSYANFPOAKSLIPLECAEDVVPDLOP  
 potapyrase 59 LHVYRPNOMLDLHIGKOVETKXIFGLSSYANFPOAKSLIPLECAEDVVPDLOP  
 mNTase 61 LHVYRPNOMLDLHIGKOVETKXIFGLSSYANFPOAKSLIPLECAEDVVPDLOP  
 yGDPase 61 LHVYRPNOMLDLHIGKOVETKXIFGLSSYANFPOAKSLIPLECAEDVVPDLOP

deaNTase 117 KTFVRLGATAGLRLNCDASEKILQVVRDNLNNSTF.NWQPDVSIINDCTOEGSYLWVT  
 potapyrase 119 KTFVRLGATAGLRLNCDASEKILQVVRDNLNNSTF.HSKDQVTLIDCTOEGSYLWVT  
 mNTase 121 KTFVRLGATAGLRLNCDASEKILQVVRDNLNNSTF.HSKDQVTLIDCTOEGSYLWVT  
 yGDPase 119 KTFVRLGATAGLRLNCDASEKILQVVRDNLNNSTF.HSKDQVTLIDCTOEGSYLWVT

deaNTase 176 VNYALGNLGRNYK..LVGVIDLGGGSVOMAYAVSKAKAKNAPKADGDPYKXKVVKQ  
 potapyrase 178 VNYALGNLGRNYK..LVGVIDLGGGSVOMAYAVSKAKAKNAPKADGDPYKXKVVKQ  
 mNTase 179 VNYALGNLGRNYK..LVGVIDLGGGSVOMAYAVSKAKAKNAPKADGDPYKXKVVKQ  
 yGDPase 179 VNYALGNLGRNYK..LVGVIDLGGGSVOMAYAVSKAKAKNAPKADGDPYKXKVVKQ

deaNTase 234 IPVULVHSYLLHGREASRAEILRL.....TPRSPHCDLACPHGIV  
 potapyrase 235 KPMVLYVHSYLLHGREASRAEILRL.....TPRSPHCDLACPHGIV  
 mNTase 232 STEKLYTHSYLLHGREASRAEILRL.....TPRSPHCDLACPHGIV  
 yGDPase 234 ENVTLYVHSYLLHGREASRAEILRL.....TPRSPHCDLACPHGIV

deaNTase 276 TVSGCEPKATAYTSGL.....NENKCKTIRANRHYPCPYCNGTEGCMWNGCGGN...  
 potapyrase 277 TVSGCEPKATAYTSGL.....NENKCKTIRANRHYPCPYCNGTEGCMWNGCGGN...  
 mNTase 270 KCFPRMLEAEWIFCGV.....KTYGCGGQGOENOTPCYAXYLRVVGQKHQPEEVR...  
 yGDPase 294 EKYTLSEKENTYIDFICGDEPSCAQCFPTDSEENKQOQSPFGSNGVHQPSLVETPK

deaNTase 328 GOKNTHASSSYLYPPEBTGHVDMSEPNFYDNFVQIEKAKACALHSDAKSRIPFDDKE  
 potapyrase 329 GOKNTHASSSYLYPPEBTGHVDMSEPNFYDNFVQIEKAKACALHSDAKSRIPFDDKE  
 mNTase 322 GSAFYAFPSYIDRAADHREIDTEKQGVLEVEPFRKAREVCHNLGPTSSCS...  
 yGDPase 354 ESNDLYIFSYFVDRTRPLCHPLFHLNPNLNDLARIKCEATKRWKVEGCHAGS...DDEL

deaNTase 388 NIASYVCMDLIYQVVLVDGCGLOLONITGKEIEYONAIIVEAANPLCNAKALSLPR  
 potapyrase 389 NIASYVCMDLIYQVVLVDGCGLOLONITGKEIEYONAIIVEAANPLCNAKALSLPR  
 mNTase 374 ....FLCMDLITVITLKDGLFAEREPLEKHESEHORDNLGLQOHSPFVSGHHQLR  
 yGDPase 411 ESNDLYIFSYFVDRTRPLCHPLFHLNPNLNDLARIKCEATKRWKVEGCHAGS...DDEL

deaNTase 448 FETCHYFV-----  
 potapyrase 448 FETCHYFV-----  
 mNTase 430 PSTGACISEPVFSQEGVDSETFSDLSGKAMPETR-  
 yGDPase 467 KCKIOGA-----

FIG. 2

[illegible][illegible][illegible][illegible]

**ACR IV**

F16.3

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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA	60
AAGACCGGCT GCCGCCTGCT CCCCAGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
GCGCGGTGCA TGGAAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA	180
AAAACGAGCT ACATTTTCA GCAGCCGAG CACGGTCCTT GGCAAACAAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG 957  
 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln  
 230 235 240

GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC 1005  
 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr  
 245 250 255

TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA 1053  
 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala  
 260 265 270

CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA 1101  
 Arg Leu Ala Ile Leu Gly Val Glu Gly Gln Pro Ala Lys Asp Gly  
 275 280 285 290

AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG 1149  
 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp  
 295 300 305

GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA 1197  
 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala  
 310 315 320

AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC 1245  
 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn  
 325 330 335

AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC 1293  
 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe  
 340 345 350

TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG 1341  
 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu  
 355 360 365 370

AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC 1389  
 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr  
 375 380 385

GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC 1437  
 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys  
 390 395 400

ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC 1485  
 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro  
 405 410 415

AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533  
 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr  
 420 425 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581  
 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg  
 435 440 445 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT 1637  
 Gln Lys Ser Pro Ala Ser  
 455

GTGTGTCTGC ATAAACCCTC CTGTCTGGA CGTGA CTCA TCCTGAGGAG CCACAGCACA 1697  
 GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC 1757  
 TGGCATCAGC CTCTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC 1817

FIG. 4 (cont'd.)

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AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCGCTCC	CGCGGCGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTCGGATGGG	AGTCTGTGCT	CCCAGCCTGT	CAGTTTCTCT	1997
CCCAGGCGAG	AGCTCCCCCT	CCTGCAAGAG	TCTGGGAGGC	GGTGAGGCT	GTCCTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGAG	AGTAGTCTG	GGCGGCACCA	2117
CTGGGAACCT	TGGACTTGAG	TGTGTTTGCT	CTTCCTGGG	TATGAATGTG	TGAGTTCAAC	2177
CAGAGGCTCG	TCTCTCTCAC	ACATTGTGTG	GTTTGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTTCAG	GAGTCTCCC	AGCATGGGCG	GATGCGGGCG	2297
ATGAGTGCT	TGAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GAGCTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACATC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGTCTGTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCCACTC	TCTCATGGAC	AGTGTTAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGGGG	GCTGAGCCCC	TTGAGTGCT	TCAGTGAATG	2657
TACAGTCCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		2762

FIG. 4 (cont'd)

Figure 1 consists of 12 sub-diagrams labeled (a) through (l), arranged vertically. Each diagram shows a different stage in the construction of a 3D model of a human head and neck. (a) shows a basic wireframe of the head and neck. (b) through (d) show the addition of facial features like eyes, nose, and mouth. (e) through (g) show the addition of hair and skin texture. (h) through (j) show the addition of clothing and accessories. (k) and (l) show the final, fully rendered model from different perspectives.



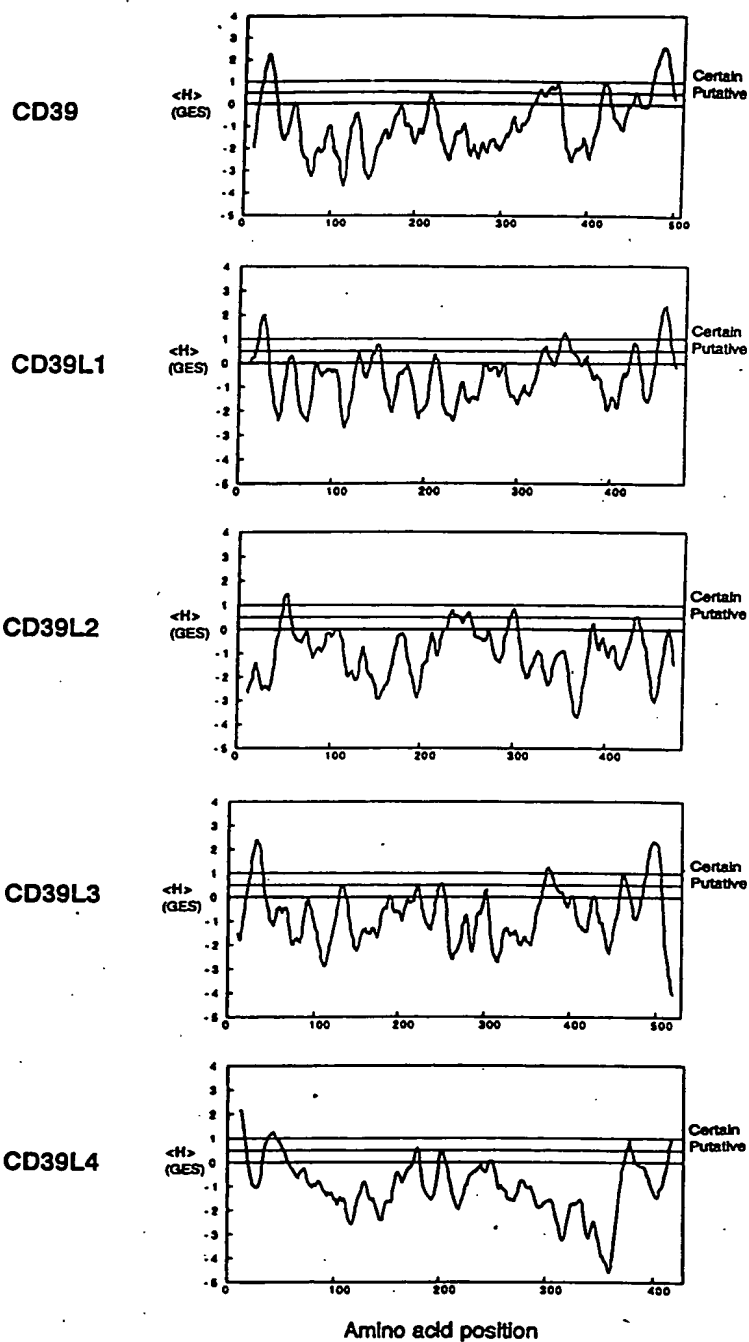


FIG. 5

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ACCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG 60  
 CTCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT 112  
 Met Phe Thr Val Leu Thr Arg Gln Pro Cys  
 1 5 10

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC 160  
 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala  
 15 20 25

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC 208  
 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val  
 30 35 40

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT 256  
 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly  
 45 50 55

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA 304  
 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln  
 60 65 70

TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC 352  
 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe  
 75 80 85 90

AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC 400  
 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro  
 95 100 105

CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG 448  
 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly  
 110 115 120

CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC 496  
 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala  
 125 130 135

ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT 544  
 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn  
 140 145 150

GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC 592 /  
 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp  
 155 160 165 170

TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA 640  
 Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly  
 175 180 185

TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG 688  
 Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu  
 190 195 200

TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG 736  
 Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu  
 205 210 215

GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG 784  
 Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys  
 220 225 230

FIG. 6

ATG Met 235	GAT Asp	CTG Leu	AAC Asn	ACC Thr	AGC Ser 240	GAC Asp	ATC Ile	ATG Met	CAG Gln 245	GTG Val	TCC Ser	CTG Leu	TAT Tyr	GGC Gly 250	TAC Tyr	832
GTA Val	TAC Tyr	ACG Thr	CTC Leu	TAC Tyr 255	ACA Thr	CAC His	AGC Ser	TTC Phe	CAG Gln 260	TGC Cys	TAT Tyr	GGC Gly	CGG Arg	AAT Asn 265	GAG Glu	880
GCT Ala	GAG Glu	AAG Lys	AAG Lys 270	TTT Phe	CTG Leu	GCA Ala	ATG Met 275	CTC Leu	CAG Gln	AAT Asn	TCT Ser	CCT Pro 280	ACC Thr	AAA Lys		928
AAC Asn	CAT His	CTC Leu 285	ACC Thr	AAT Asn	CCC Pro	TGT Cys	TAC Tyr 290	CCT Pro	CGG Arg	GAT Asp	TAT Tyr	AGC Ser 295	ATC Ile	AGC Ser	TTC Phe	976
ACC Thr 300	ATG Met	GGC Gly	CAT His	GTA Val	TTT Phe 305	GAT Asp 305	AGC Ser	CTG Leu	TGC Cys	ACT Thr	GTG Val 310	GAC Asp	CAG Gln	AGG Arg	CCA Pro	1024
GAA Glu 315	AGT Ser	TAT Tyr	AAC Asn	CCC Pro	AAT Asp 320	GAT Asp	GTC Val	ATC Ile	ACT Thr	TTT Phe 325	GAA Glu	GGA Gly	ACT Thr	GGG Gly	GAC Asp 330	1072
CCA Pro	TCT Ser	CTG Leu	TGT Cys	AAG Lys 335	GAG Glu	AAG Lys	GTG Val	GCT Ala	TCC Ser	ATA Ile	TTT Phe	GAC Asp	TTC Phe	AAA Lys 345	GCT Ala	1120
TGC Cys	CAT His	GAT Asp 350	CAA Gln	GAA Glu	ACC Thr	TGT Cys	TCT Ser 355	TTT Phe	GAT Asp	GGG Gly	GTT Val	TAT Tyr	CAG Gln 360	CCA Pro	AAG Lys	1168
ATT Ile	AAA Lys 365	GGG Pro	CCA Phe	TTT Phe	GTG Val	GCT Ala	TTT Phe 370	GCA Ala	GGA Gly	TTC Phe	TAC Tyr	TAC Tyr	ACA Thr	GCC Ala	AGT Ser	1216
GCT Ala 380	TTA Leu	AAT Asn	CTT Leu	TCA Ser	GGT Gly	AGC Ser 385	TTT Phe	TCC Ser	CTG Leu	GAC Asp	ACC Thr 390	TTC Phe	AAC Asn	TCC Ser	AGC Ser	1264
ACC Thr 395	TGG Trp	AAT Asn	TTC Phe	TGC Cys	TCA Ser 400	CAG Gln	AAT Asn	TGG Trp	AGT Ser	CAG Gln 405	CTC Leu	CCA Pro	CTG Leu	CTG Leu 410	CTC Leu	1312
CCC Pro	AAA Lys	TTT Phe	GAT Asp 415	GAG Glu	GTA Val	TAT Tyr	GCC Ala	CGC Arg	TCT Ser 420	TAC Tyr	TGC Cys	TTC Phe	TCA Ser	GCC Ala 425	AAC Asn	1360
TAC Tyr	ATC Ile	TAC Tyr	CAC His 430	TTG Leu	TTT Phe	GTG Val	AAC Asn 435	GGT Gly	TAC Tyr	AAA Lys	TTC Phe	ACA Thr	GAG Glu 440	GAG Glu	ACT Thr	1408
TGG Trp	CCC Pro	CAA Gln 445	ATA Ile	CAC His	TTT Phe	GAA Glu	AAA Lys 450	GAA Glu	GTG Val	GGG Gly	AAT Asn 455	AGC Ser	AGC Ser	ATA Ile	GCC Ala	1456
TGG Trp	TCT Ser 460	CTT Leu	GGC Gly	TAC Tyr	ATG Met	CTC Leu 465	AGC Ser	CTG Leu	ACC Thr	AAC Asn	CAG Gln 470	ATC Ile	CCA Pro	GCT Ala	GAA Glu	1504
AGC Ser 475	CCT Pro	CTG Leu	ATC Ile	CGT Arg	CTG Leu 480	CCC Pro	ATA Ile	GAA Glu	CCA Pro	CCT Pro 485	GTC Val	TTT Phe	GTG Val	GGC Gly	ACC Thr 490	1552

FIG. 6 (cont'd.)

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CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600  
 Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala  
 495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648  
 Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe  
 510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC 1703  
 Asp His Ala Val Asp Ser Asp  
 525

TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA 1763  
 TACAACCTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC 1823  
 AGCACCTCTT GAGGCATCCC TTGGCTATTG TGTGCATATT GTTCTTCAGA GACCTCACTA 1883  
 CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA 1943  
 TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG 2003  
 ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA 2063  
 AGCATTTTCG CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT 2123  
 TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG 2183  
 GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA 2243  
 TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG 2303  
 GAATTTCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTC ATCATCCTCA 2363  
 TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT 2423  
 GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT 2483  
 GTTATCATGG TGTATATATT TTTGTCAACCA TTCCCAACAG TATACTTGAT GTTGTCTAG 2543  
 AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT 2603  
 GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTATC 2663  
 TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAACTA AAAATCAGCA 2723  
 TTATTTTATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTTGA 2783  
 AAAAAAAAAA AAAA 2797

FIG. 6 (cont.d.)

GCGCGCGCGT	TTTCCTTGTT	CCTGGTCAAC	AAAGAAATGT	GGAGTGTCTT	GGCTGAATCC	60
TCATACAGAC	AAGATCATT	TGGTGCTGTT	AGGTAGGACT	TGTATCCAGA	TGTAAGGTTG	120
AAAAAGTGAT	ATAATAAAGG	AACCAAGGAG	AAAATTCAGA	AGGAAAGAAA	AAATTGCCTC	180
TGCAGGTGTG	CGAGCAGGAT	TGCTTCTGCA	ACAAAAGCCT	CCACCCAGCC	ACATCTTGGG	240
AAAAGA ATG	GCC ACT TCT	TGG GGC ACA	GTC TTT TTC	ATG CTG GTG	GTA	288
Met	Ala Thr Ser Trp	Gly Thr Val Phe	Phe Met Leu Val	Val		
1		5		10		
TCC TGT GTT	TGC AGC GCT	GTC TCC CAC	AGG AAC CAG	CAG ACT TGG	TTT	336
Ser Cys Val	Cys Ser Ala	Val Ser His	Arg Asn Gln	Gln Thr Trp	Phe	
15		20		25	30	
GAG GGT ATC	TTC CTG TCT	TCC ATG TGC	CCC ATC AAT	GTC AGC GCC	AGC	384
Glu Gly Ile	Phe Leu Ser	Ser Met Cys	Pro Ile Asn	Val Ser Ala	Ser	
	35		40		45	
ACC TTG TAT	GGA ATT ATG	TTT GAT GCA	GGG AGC ACT	GGA ACT CGA	ATT	432
Thr Leu Tyr	Gly Ile Met	Phe Asp Ala	Gly Ser Thr	Gly Thr Arg	Ile	
	50		55		60	
CAT GTT TAC	ACC TTT GTG	CAG AAA ATG	CCA GGA CAG	CTT CCA ATT	CTA	480
His Val Tyr	Thr Phe Val	Gln Lys Met	Pro Gly Gln	Leu Pro Ile	Leu	
	65		70		75	
GAA GGG GAA	GTT TTT GAT	TCT GTG AAG	CCA GGA CTT	TCT GCT TTT	GTA	528
Glu Gly Glu	Val Phe Asp	Ser Val Lys	Pro Gly Leu	Ser Ala Phe	Val	
	80		85		90	
GAT CAA CCT	AAG CAG GGT	GCT GAG ACC	GTT CAA GGG	CTC TTA GAG	GTG	576
Asp Gln Pro	Lys Gln Gly	Ala Glu Thr	Val Gln Gly	Leu Leu Glu	Val	
	95		100		105	110
GCC AAA GAC	TCA ATC CCC	CGA AGT CAC	TGG AAA AAG	ACC CCA GTG	GTC	624
Ala Lys Asp	Ser Ile Pro	Arg Ser His	Trp Lys Lys	Thr Pro Val	Val	
	115		120		125	
CTA AAG GCA	ACA GCA GGA	CTA CGC TTA	CTG CCA GAA	CAC AAA GCC	AAG	672
Leu Lys Ala	Thr Ala Gly	Leu Arg Leu	Pro Glu His	Lys Ala Lys		
	130		135		140	
GCT CTG CTC	TTT GAG GTA	AAG GAG ATC	TTC AGG AAG	TCA CCT TTC	CTG	720
Ala Leu Leu	Phe Glu Val	Lys Glu Ile	Phe Arg Lys	Ser Pro Phe	Leu	
	145		150		155	
GTA CCA AAG	GGC AGT GTT	AGC ATC ATG	GAT GGA TCC	GAC GAA GGC	ATA	768
Val Pro Lys	Gly Ser Val	Ser Ile Met	Asp Gly Ser	Asp Glu Gly	Ile	
	160		165		170	
TTA GCT TGG	GTT ACT GTG	AAT TTT CTG	ACA GGT CAG	CTG CAT GGC	CAC	816
Leu Ala Trp	Val Thr Val	Asn Phe Leu	Thr Gly Gln	Leu His Gly	His	
	175		180		185	190
AGA CAG GAG	ACT GTG GGG	ACC TTG GAC	CTA GGG GGA	GCC TCC ACC	CAA	864
Arg Gln Glu	Thr Val Gly	Thr Leu Asp	Leu Gly Gly	Ala Ser Thr	Gln	
	195		200		205	
ATC ACG TTC	CTG CCC CAG	TTT GAG AAA	ACT CTG GAA	CAA ACT CCT	AGG	912
Ile Thr Phe	Leu Pro Gln	Phe Glu Lys	Thr Leu Glu	Gln Thr Pro	Arg	
	210		215		220	
GGC TAC CTC	ACT TCC TTT	GAG ATG TTT	AAC AGC ACT	TAT AAG CTC	TAT	960
Gly Tyr Leu	Thr Ser Phe	Glu Met Phe	Asn Ser Thr	Tyr Lys Leu	Tyr	
	225		230		235	

FIG. 7

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	
290 295 300	
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	
335 340 345 350	
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG	1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu	
355 360 365	
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370 375 380	
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC	1539
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG	1599
TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT	1659
TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA	1719
TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC	1779
CCAGGGACAG GTCCTGGAA ACCAAAGAAA AATCGCATT CAACCCTTG AGTGCCTCAT	1839
TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAACTG ACTTATTGCA ATCCCAAGAC	1899
CCATCAATAT CAGTATTTTT TTCCTCCCTA TACAGTGCCC TGCCCACCCT TATCTGCACC	1959
CACCTCCCT GAAAAAGAGA GAAAAAATAAAAAA	1998

Fig. 7 (cont'd.)

CD39L2 1 MKKGIATYTSRRTSYIFQOPQHGPWQTRMKKISNHOGLAVAKVATPLGCVGVYHYVATN  
 CD39L4 1 .....  
 CD39L1 1 .....  
 CD39L3 1 .....  
 CD39 1 .....  
 ACR I  
 CD39L2 61 SNWETATACQFPTFATRAPTFACGCAK.FPLGTAAGHGVFYGIE DAGSGCTFVAVLO  
 CD39L4 7 TVPMLLVVSCCSASRRHOOTFPGFESSMCPFVSARTLYGIE DAGSGCTFVAVLO  
 CD39L1 1 .....  
 CD39L3 16 KATYRFPITIALVYLLSIVLVSTIAGIKKVLPPKVKYIVLDAGSSHTSVYVVO  
 CD39 7 SNWETATACQFPTFATRAPTFACGCAK.FPLGTAAGHGVFYGIE DAGSGCTFVAVLO  
 ACR II  
 CD39L2 120 FT.RPFRPTTBEZKVN.PC.SAYADVKKAOEELVAVKODITFDPMKRIE  
 CD39L4 67 FVOKKPGOLFICEVDSVLDGSAVDGPKAFAGGOLLEVAHDSIPRSMMKRIE  
 CD39L1 58 NPAKENDTGIVGCEHCEVPCGSSVADHPSCNOLVCGCEQADDPREHMAITPL  
 CD39L3 75 NPAKENDTGIVGCEHCEVPCGSSVADHPSCNOLVCGCEQADDPREHMAITPL  
 CD39 67 NPAKENDTGIVGCEHCEVPCGSSVADHPSCNOLVCGCEQADDPREHMAITPL  
 ACR II  
 CD39L2 178 PLATAGKLL...GKNA...LKKNEKNSPLLVGDDCVSINCTECUGKILID  
 CD39L4 126 PLATAGKLL...GKNA...LKKNEKNSPLLVGDDCVSINCTECUGKILID  
 CD39L1 114 PLGATACHRLLETHFAITSLVMVYTLTQYFF..DFRGARIPSGOECGVGHTANN  
 CD39L3 135 PLGATACHRLLETHFAITSLVMVYTLTQYFF..DFRGARIPSGOECGVGHTANN  
 CD39 127 PLGATACHRLLETHFAITSLVMVYTLTQYFF..DFRGARIPSGOECGVGHTANN  
 ACR III  
 CD39L2 235 STSL.....STPGGSLVGLDLSG-STGIFLPRVETALASPPSYLTALRE  
 CD39L4 183 STSL.....STPGGSLVGLDLSG-STGIFLPRVETALASPPSYLTALRE  
 CD39L1 176 STSL.....STPGGSLVGLDLSG-STGIFLPRVETALASPPSYLTALRE  
 CD39L3 193 STSL.....STPGGSLVGLDLSG-STGIFLPRVETALASPPSYLTALRE  
 CD39 185 STSL.....STPGGSLVGLDLSG-STGIFLPRVETALASPPSYLTALRE  
 ACR IV  
 CD39L2 283 NRTYKLYTSHLGLGLMGLARLALGATGCPKPCGMLVSPCLSPSPKEMERVAVR  
 CD39L4 231 NRTYKLYTSHLGLGLMGLARLALGATGCPKPCGMLVSPCLSPSPKEMERVAVR  
 CD39L1 229 YGQHYRVTYHSLFLCYGRDQVLOREASAG...TQFHPGMPRGFS...TVLGDVYOS  
 CD39L3 248 YGQHYRVTYHSLFLCYGRDQVLOREASAG...TQFHPGMPRGFS...TVLGDVYOS  
 CD39 242 YGQHYRVTYHSLFLCYGRDQVLOREASAG...TQFHPGMPRGFS...TVLGDVYOS  
 CD39L2 343 YGQKAAASREBLAARNSVQHRFRTSEV...DYAFSYYIDLAHOVSHALKGGS  
 CD39L4 290 YGQKAAASREBLAARNSVQHRFRTSEV...DYAFSYYIDLAHOVSHALKGGS  
 CD39L1 283 YGQKAAASREBLAARNSVQHRFRTSEV...DYAFSYYIDLAHOVSHALKGGS  
 CD39L3 307 LNTVDORPESKMDVTFECTHNSLSEKMSHDKACHDO...TFEFGVGEQKIKP  
 CD39 300 LNTVDORPESKMDVTFECTHNSLSEKMSHDKACHDO...TFEFGVGEQKIKP  
 CD39L2 403 LNVCOPEIRAKTYCALETQOSSPFSNDAYVLLLOK.FEPRSKVEMKTERNDIVE  
 CD39L4 350 LNVCOPEIRAKTYCALETQOSSPFSNDAYVLLLOK.FEPRSKVEMKTERNDIVE  
 CD39L1 342 NV.....AFSAFYVYASALNLSGSE...STPTFESTHETGONKSOPLSLTFFDHY  
 CD39L3 367 NV.....AFSAFYVYASALNLSGSE...STPTFESTHETGONKSOPLSLTFFDHY  
 CD39 357 NV.....AFSAFYVYASALNLSGSE...STPTFESTHETGONKSOPLSLTFFDHY  
 CD39L2 462 SSALCALSHYDSGKSPSG\*.....  
 CD39L4 410 SSALCALSHYDSGKSPSG\*.....  
 CD39L1 384 .....  
 CD39L3 418 LSETCY...TITLISLGLCGYHPTAGKRIIFICGQSDALGCVHHLTHIPAEQD  
 CD39 409 LSETCY...TITLISLGLCGYHPTAGKRIIFICGQSDALGCVHHLTHIPAEQD  
 CD39L2 485 .....  
 CD39L4 429 .....  
 CD39L1 432 .....  
 CD39L3 476 .....  
 CD39 466 .....  
 ACR I  
 ACR II  
 ACR III  
 ACR IV

Fig. 8

peaGDP 1  
 potapyrase 1  
 CD39L2 1  
 CD39L4 1  
 dNTPase 1  
 yGDPase 1

peaGDP 2  
 potapyrase 6  
 CD39L2 61  
 CD39L4 7  
 dNTPase 37  
 yGDPase 5

peaGDP 61  
 potapyrase 63  
 CD39L2 119  
 CD39L4 66  
 dNTPase 96  
 yGDPase 65

peaGDP 121  
 potapyrase 123  
 CD39L2 178  
 CD39L4 126  
 dNTPase 156  
 yGDPase 123

peaGDP 180  
 potapyrase 182  
 CD39L2 236  
 CD39L4 184  
 dNTPase 214  
 yGDPase 183

peaGDP 238  
 potapyrase 239  
 CD39L2 289  
 CD39L4 237  
 dNTPase 264  
 yGDPase 238

peaGDP 276  
 potapyrase 277  
 CD39L2 335  
 CD39L4 282  
 dNTPase 308  
 yGDPase 298

peaGDP 332  
 potapyrase 333  
 CD39L2 379  
 CD39L4 326  
 dNTPase 360  
 yGDPase 358

peaGDP 392  
 potapyrase 392  
 CD39L2 428  
 CD39L4 375  
 dNTPase 406  
 yGDPase 415

peaGDP 452  
 potapyrase 452  
 CD39L2 483  
 CD39L4 429  
 dNTPase 462  
 yGDPase 471